

## SEQUENCE LISTING

<110> Fox, Brian  
Holloway, James L.

<120> ADIPOCYTE COMPLMENT RELATED PROTEIN  
ZACRP13

<130> 00-96C1

<150> US 09/997,610

<151> 2001-11-29

<150> US 60/253,924

<151> 2000-11-29

<160> 7

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1381

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2)...(1381)

<400> 1

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     1             5             10             15

gtt gct gga cct cca gca cac ccc agg ccc cca gaa gaa gtg ggg cct 97
Val Ala Gly Pro Pro Ala His Pro Arg Pro Pro Glu Glu Val Gly Pro
      20             25             30

cct ggt gca cca ggt tta cca caa tat aca gga gaa ata agt gaa atg 145
Pro Gly Ala Pro Gly Leu Pro Gln Tyr Thr Gly Glu Ile Ser Glu Met
      35             40             45

aca aaa tgc ccc tgt cct gat ata gaa agg tca gcc ttt act gtg aag 193
Thr Lys Cys Pro Cys Pro Asp Ile Glu Arg Ser Ala Phe Thr Val Lys
      50             55             60

ctc agt gga aaa ctt cct ctt cct ttc aag ccc atc atc ttc aca ggg 241
Leu Ser Gly Lys Leu Pro Leu Pro Phe Lys Pro Ile Ile Phe Thr Gly
      65             70             75             80

gtc ctg tac aat gcc cag agg gat tta aag gag gcc atg gga gtc ttt 289
Val Leu Tyr Asn Ala Gln Arg Asp Leu Lys Glu Ala Met Gly Val Phe
      85             90             95

gct tgc agg gtg cct ggg aat tac tac tcc agc ttt gat gtt gag ctg 337
Ala Cys Arg Val Pro Gly Asn Tyr Tyr Ser Ser Phe Asp Val Glu Leu
      100            105            110

cat cat tgc aag gtg aat att tgg cta atg agg aag caa att ttg gct 385
His His Cys Lys Val Asn Ile Trp Leu Met Arg Lys Gln Ile Leu Ala
      115            120            125

aat aag gaa gaa att tct aag cag caa agc att caa gag gtg act tgg 433
Asn Lys Glu Glu Ile Ser Lys Gln Gln Ser Ile Gln Glu Val Thr Trp

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130	135	140	
gtg ctg tta aag gca ttc agt ttc ata agg gag gca gag cat aag agt			481
Val Leu Leu Lys Ala Phe Ser Phe Ile Arg Glu Ala Glu His Lys Ser			
145	150	155	160
tca gaa aat ttg cac cct gac aat gtg ata aaa aag aaa aac cca ttt			529
Ser Glu Asn Leu His Pro Asp Asn Val Ile Lys Lys Lys Asn Pro Phe			
	165	170	175
tct gag ggg aaa ttc aag ctg gct gca gaa att tgc ata tgt aat gag			577
Ser Glu Gly Lys Phe Lys Leu Ala Ala Glu Ile Cys Ile Cys Asn Glu			
	180	185	190
gag ctg aat gtt aat cct caa gac aat ggg gaa aat atc tcc tgg aca			625
Glu Leu Asn Val Asn Pro Gln Asp Asn Gly Glu Asn Ile Ser Trp Thr			
	195	200	205
tgt cag agg tct tca cag cag tcc atc aaa tca ctg gcc tgg agg cct			673
Cys Gln Arg Ser Ser Gln Gln Ser Ile Lys Ser Leu Ala Trp Arg Pro			
	210	215	220
agg aga aaa tgg ttt tgt ggg aca ggc cca ggg tcc ctg tgc tgt gtg			721
Arg Arg Lys Trp Phe Cys Gly Thr Gly Pro Gly Ser Leu Cys Cys Val			
	225	230	235
cag cct aga gac ttg gtg ccc tgt gtc cca gtt aat tca gct gtg gct			769
Gln Pro Arg Asp Leu Val Pro Cys Val Pro Val Asn Ser Ala Val Ala			
	245	250	255
tca gag ggt gca agc ccc aag cct tgg cag ctt cca agt ggt gtt gag			817
Ser Glu Gly Ala Ser Pro Lys Pro Trp Gln Leu Pro Ser Gly Val Glu			
	260	265	270
cct gtg ggt gca aag aag tca aga att gag gtt tgg gaa cct cca atc			865
Pro Val Gly Ala Lys Lys Ser Arg Ile Glu Val Trp Glu Pro Pro Ile			
	275	280	285
aga ttt cag aag ata tat gga aac ccc tgg atg ccc agg cag aag ttt			913
Arg Phe Gln Lys Ile Tyr Gly Asn Pro Trp Met Pro Arg Gln Lys Phe			
	290	295	300
gct gta ggg gtg ggg tcc tca tgg aga acc tct gca agg gta gta caa			961
Ala Val Gly Val Gly Ser Ser Trp Arg Thr Ser Ala Arg Val Val Gln			
	305	310	315
aag gga aat gtt ggg tgg gag ccc cca cac aga gtc ccc agt ggg gct			1009
Lys Gly Asn Val Gly Trp Glu Pro Pro His Arg Val Pro Ser Gly Ala			
	325	330	335
cca tct agt aga gct gtg aga aga agt cca cca tcc tcc aga ctc cag			1057
Pro Ser Ser Arg Ala Val Arg Arg Ser Pro Pro Ser Ser Arg Leu Gln			
	340	345	350
aag ggt aga tcc act gac agc ttg cag cat gtg cct gaa aaa tcc aca			1105
Lys Gly Arg Ser Thr Asp Ser Leu Gln His Val Pro Glu Lys Ser Thr			
	355	360	365
gac act cag tgc cag cct gtg aaa gca gca ggg atg gag tct gta ccc			1153
Asp Thr Gln Cys Gln Pro Val Lys Ala Ala Gly Met Glu Ser Val Pro			
	370	375	380
tac aaa acc gta gtg gca gag ctg acc aag acc gtg gga atc tac ctc			1201
Tyr Lys Thr Val Val Ala Glu Leu Thr Lys Thr Val Gly Ile Tyr Leu			

385	390	395	400	
ttg cat tgt cat gac ctg gac gtg aga cat gga gtc aaa aga gat cat				1249
Leu His Cys His Asp Leu Asp Val Arg His Gly Val Lys Arg Asp His				
	405	410	415	
ttt gga gct tta aga ttt gac tgc ccc act gga ttt cgg act tat atg				1297
Phe Gly Ala Leu Arg Phe Asp Cys Pro Thr Gly Phe Arg Thr Tyr Met				
	420	425	430	
ggg ccc gta ccc ctt tgt ttt ggc caa ttt ttt cca ttt gga act gcc				1345
Gly Pro Val Pro Leu Cys Phe Gly Gln Phe Phe Pro Phe Gly Thr Ala				
	435	440	445	
gta ttt acc caa tgc ctg tac ctc cat tgt atg tag				1381
Val Phe Thr Gln Cys Leu Tyr Leu His Cys Met *				
	450	455		

<210> 2  
 <211> 459  
 <212> PRT  
 <213> Homo sapiens

<400> 2  
 Ile Val Val Ile Pro Val Leu Ile Thr Ala Val Ile Glu His Val Glu  
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 Val Ala Gly Pro Pro Ala His Pro Arg Pro Pro Glu Glu Val Gly Pro  
 20 25 30  
 Pro Gly Ala Pro Gly Leu Pro Gln Tyr Thr Gly Glu Ile Ser Glu Met  
 35 40 45  
 Thr Lys Cys Pro Cys Pro Asp Ile Glu Arg Ser Ala Phe Thr Val Lys  
 50 55 60  
 Leu Ser Gly Lys Leu Pro Leu Pro Phe Lys Pro Ile Ile Phe Thr Gly  
 65 70 75 80  
 Val Leu Tyr Asn Ala Gln Arg Asp Leu Lys Glu Ala Met Gly Val Phe  
 85 90 95  
 Ala Cys Arg Val Pro Gly Asn Tyr Tyr Ser Ser Phe Asp Val Glu Leu  
 100 105 110  
 His His Cys Lys Val Asn Ile Trp Leu Met Arg Lys Gln Ile Leu Ala  
 115 120 125  
 Asn Lys Glu Glu Ile Ser Lys Gln Gln Ser Ile Gln Glu Val Thr Trp  
 130 135 140  
 Val Leu Leu Lys Ala Phe Ser Phe Ile Arg Glu Ala Glu His Lys Ser  
 145 150 155 160  
 Ser Glu Asn Leu His Pro Asp Asn Val Ile Lys Lys Lys Asn Pro Phe  
 165 170 175  
 Ser Glu Gly Lys Phe Lys Leu Ala Ala Glu Ile Cys Ile Cys Asn Glu  
 180 185 190  
 Glu Leu Asn Val Asn Pro Gln Asp Asn Gly Glu Asn Ile Ser Trp Thr  
 195 200 205  
 Cys Gln Arg Ser Ser Gln Gln Ser Ile Lys Ser Leu Ala Trp Arg Pro  
 210 215 220  
 Arg Arg Lys Trp Phe Cys Gly Thr Gly Pro Gly Ser Leu Cys Cys Val  
 225 230 235 240  
 Gln Pro Arg Asp Leu Val Pro Cys Val Pro Val Asn Ser Ala Val Ala  
 245 250 255  
 Ser Glu Gly Ala Ser Pro Lys Pro Trp Gln Leu Pro Ser Gly Val Glu  
 260 265 270  
 Pro Val Gly Ala Lys Lys Ser Arg Ile Glu Val Trp Glu Pro Pro Ile  
 275 280 285  
 Arg Phe Gln Lys Ile Tyr Gly Asn Pro Trp Met Pro Arg Gln Lys Phe  
 290 295 300  
 Ala Val Gly Val Gly Ser Ser Trp Arg Thr Ser Ala Arg Val Val Gln

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305          310          315          320
Lys Gly Asn Val Gly Trp Glu Pro Pro His Arg Val Pro Ser Gly Ala
          325          330          335
Pro Ser Ser Arg Ala Val Arg Arg Ser Pro Pro Ser Ser Arg Leu Gln
          340          345          350
Lys Gly Arg Ser Thr Asp Ser Leu Gln His Val Pro Glu Lys Ser Thr
          355          360          365
Asp Thr Gln Cys Gln Pro Val Lys Ala Ala Gly Met Glu Ser Val Pro
          370          375          380
Tyr Lys Thr Val Val Ala Glu Leu Thr Lys Thr Val Gly Ile Tyr Leu
385          390          395          400
Leu His Cys His Asp Leu Asp Val Arg His Gly Val Lys Arg Asp His
          405          410          415
Phe Gly Ala Leu Arg Phe Asp Cys Pro Thr Gly Phe Arg Thr Tyr Met
          420          425          430
Gly Pro Val Pro Leu Cys Phe Gly Gln Phe Phe Pro Phe Gly Thr Ala
          435          440          445
Val Phe Thr Gln Cys Leu Tyr Leu His Cys Met
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<210> 3
<211> 1377
<212> DNA
<213> Artificial Sequence

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<220>
<223> Degenerate polynucleotide encoding a polypeptide
      of SEQ ID NO:2

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<221> variation
<222> (1)...(1377)
<223> Each n is independently A, T, G, or C.

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<221> misc_feature
<222> (1)...(1377)
<223> n = A,T,C or G

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<400> 3
athgtngtna thccngtnyt nathacngcn gtnathgarc aygtngargt ngcnggnccn 60
ccngcncayc cnmgnccncc ngargargtn ggncncncng gngcncncng nytnccncar 120
tayacnggng arathwsnga ratgacnaar tgyccntgyc cngayathga rmgnwsngcn 180
ttyacngtna arytnwsngg naarytnccn ytnccnttya arccnathat httyacnggn 240
gtnytnaya aygncarmg ngayytnaar gargcnatgg gngtnttygc ntgymgngtn 300
ccnggnaayt aytaywsnws nttygaygtg garytncayc aytgyaargt naayathtg 360
ytnatgmgn aarcathyt ngcnaayaar gargarathw snaarcarca rwsnathcar 420
gargtnacnt gggtnytnyt naargcntty wsnttyathm gngargcnga rcayaarwsn 480
wsngaraayy tncayccnga yaaygttnath aaraaraara ayccnttyws ngarggnaar 540
ttyaarytng cngcngarat htgyathtgy aaygargary tnaaygtnaa yccncargay 600
aayggngara ayathwsntg gacntgycar mgnwsnwsnc arcarwsnat haarwsnytn 660
gcntggmgnc cnmgnmgnaa rtggttytgy ggnacnggnc cnggnwsnyt ntgytgygt 720
carccnmgng ayytngtncc ntgygtncn gtnaaywsng cngtngcnws ngarggngcn 780
wsnccnaarc cntggcaryt nccnwsnggn gtngarccng tnggngcnaa raarwsnmgn 840
athgargtnat gggarccncc nathmgntty caraaratht ayggnaaycc ntggatgccn 900
mgncaraart tygcngtngg ngtnngnwsn wsntggmgna cnwsngcnmg ngtngtncar 960
aarggnaayg tnggntggga rccncncay mgngtnccnw snggngcncc nwsnwsnmgn 1020
gcngtnmgm gnwsncncc nwsnwsnmgn ytncaraarg gnmgnwsnac ngaywsnytn 1080
carcaygtnc cngaraarws nacngayacn cartgycarc cngtnaargc ngcnggnatg 1140
garwsngtn cntayaarac ngtngtngcn garytnacna aracngtngg nathtayytn 1200
ytncaytgyc aygayytnga ygtngmncay ggngtnaarm gngaycaytt yggngcnytn 1260
mgnttygayt gyccnacngg nttymgnaen tayatgggnc cngtnccnyt ntgyttygg 1320
carttyttyp cnttyggnac ngcngtnntt acncartggy tntayytnca ytgyatg 1377

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<210> 4

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<211> 31  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Aromatic motif

<221> VARIANT  
 <222> (2)...(6)  
 <223> Each Xaa is any amino acid residue

<221> VARIANT  
 <222> (7)...(7)  
 <223> Xaa is asparagine or aspartic acid

<221> VARIANT  
 <222> (8)...(11)  
 <223> Each Xaa is independently any amino acid residue

<221> VARIANT  
 <222> (12)...(12)  
 <223> Xaa is phenylalanine, tyrosine, tryptophan, or leucine

<221> VARIANT  
 <222> (13)...(18)  
 <223> Each Xaa is independently any amino acid residue

<221> VARIANT  
 <222> (20)...(24)  
 <223> Each Xaa is independently any amino acid residue

<221> VARIANT  
 <222> (26)...(26)  
 <223> Xaa is any amino acid residue

<221> VARIANT  
 <222> (28)...(31)  
 <223> Each Xaa is independently any amino acid residue

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 Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa Gly Xaa Tyr Xaa Xaa Xaa Xaa  
 20 25 30

<210> 5  
 <211> 1731  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(1731)

<400> 5  
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 Met Leu Ile Glu Ala Tyr Gly Gly Asp Leu Val Ala Gln Gly Ser Lys  
 1 5 10 15  
 aaa tgc tgc att gga gag atg ggg tac atg cga gtg aca atg gga aga 96  
 Lys Cys Cys Ile Gly Glu Met Gly Tyr Met Arg Val Thr Met Gly Arg

20	25	30	
gtt ggt agc tgg aga gaa ctg gga aag cct tca ggc atc tgg gaa atg Val Gly Ser Trp Arg Glu Leu Gly Lys Pro Ser Gly Ile Trp Glu Met 35 40 45			144
gct ggg gat aca gag gtg aag aag aca ggg ttt ctt cag gaa ctc act Ala Gly Asp Thr Glu Val Lys Lys Thr Gly Phe Leu Gln Glu Leu Thr 50 55 60			192
ttc cag cag gag cct ggc atc tcc tcc tct cct tct tgc tcc cgc tct Phe Gln Gln Glu Pro Gly Ile Ser Ser Ser Pro Ser Cys Ser Arg Ser 65 70 75 80			240
tgc cat gtg aca cca cct gct cca cct gca tct tct gcc ata att gta Cys His Val Thr Pro Ala Pro Pro Ala Ser Ser Ala Ile Ile Val 85 90 95			288
aga ttc ctg agg ccc tca cca gaa gca gat gcc agc agc atg ctt att Arg Phe Leu Arg Pro Ser Pro Glu Ala Asp Ala Ser Ser Met Leu Ile 100 105 110			336
gca cag tct gta gaa ccg ata gtg gtc ata cct gtc tta ata acg gca Ala Gln Ser Val Glu Pro Ile Val Val Ile Pro Val Leu Ile Thr Ala 115 120 125			384
gtc att gag cat gta gaa gtt gct gga cct cca gca cac ccc agg ccc Val Ile Glu His Val Glu Val Ala Gly Pro Pro Ala His Pro Arg Pro 130 135 140			432
cca gaa gaa gtg ggg cct cct ggt gca cca ggt tta cca caa tat aca Pro Glu Glu Val Gly Pro Pro Gly Ala Pro Gly Leu Pro Gln Tyr Thr 145 150 155 160			480
gga gaa ata agt gaa atg aca aaa tgc ccc tgt cct gat ata gaa agg Gly Glu Ile Ser Glu Met Thr Lys Cys Pro Cys Pro Asp Ile Glu Arg 165 170 175			528
tca gcc ttt act gtg aag ctc agt gga aaa ctt cct ctt cct ttc aag Ser Ala Phe Thr Val Lys Leu Ser Gly Lys Leu Pro Leu Pro Phe Lys 180 185 190			576
ccc atc atc ttc aca ggg gtc ctg tac aat gcc cag agg gat tta aag Pro Ile Ile Phe Thr Gly Val Leu Tyr Asn Ala Gln Arg Asp Leu Lys 195 200 205			624
gag gcc atg gga gtc ttt gct tgc agg gtg cct ggg aat tac tac tcc Glu Ala Met Gly Val Phe Ala Cys Arg Val Pro Gly Asn Tyr Tyr Ser 210 215 220			672
agc ttt gat gtt gag ctg cat cat tgc aag gtg aat att tgg cta atg Ser Phe Asp Val Glu Leu His His Cys Lys Val Asn Ile Trp Leu Met 225 230 235 240			720
agg aag caa att ttg gct aat aag gaa gaa att tct aag cag caa agc Arg Lys Gln Ile Leu Ala Asn Lys Glu Glu Ile Ser Lys Gln Gln Ser 245 250 255			768
att caa gag gtg act tgg gtg ctg tta aag gca ttc agt ttc ata agg Ile Gln Glu Val Thr Trp Val Leu Leu Lys Ala Phe Ser Phe Ile Arg 260 265 270			816
gag gca gag cat aag agt tca gaa aat ttg cac cct gac aat gtg ata Glu Ala Glu His Lys Ser Ser Glu Asn Leu His Pro Asp Asn Val Ile			864

275	280	285	
aaa aag aaa aac cca ttt tct gag ggg aaa ttc aag ctg gct gca gaa Lys Lys Lys Asn Pro Phe Ser Glu Gly Lys Phe Lys Leu Ala Ala Glu 290 295 300			912
att tgc ata tgt aat gag gag ctg aat gtt aat cct caa gac aat ggg Ile Cys Ile Cys Asn Glu Glu Leu Asn Val Asn Pro Gln Asp Asn Gly 305 310 315 320			960
gaa aat atc tcc tgg aca tgt cag agg tct tca cag cag tcc atc aaa Glu Asn Ile Ser Trp Thr Cys Gln Arg Ser Ser Gln Gln Ser Ile Lys 325 330 335			1008
tca ctg gcc tgg agg cct agg aga aaa tgg ttt tgt ggg aca ggc cca Ser Leu Ala Trp Arg Pro Arg Arg Lys Trp Phe Cys Gly Thr Gly Pro 340 345 350			1056
ggg tcc ctg tgc tgt gtg cag cct aga gac ttg gtg ccc tgt gtc cca Gly Ser Leu Cys Cys Val Gln Pro Arg Asp Leu Val Pro Cys Val Pro 355 360 365			1104
gtt aat tca gct gtg gct tca gag ggt gca agc ccc aag cct tgg cag Val Asn Ser Ala Val Ala Ser Glu Gly Ala Ser Pro Lys Pro Trp Gln 370 375 380			1152
ctt cca agt ggt gtt gag cct gtg ggt gca aag aag tca aga att gag Leu Pro Ser Gly Val Glu Pro Val Gly Ala Lys Lys Ser Arg Ile Glu 385 390 395 400			1200
gtt tgg gaa cct cca atc aga ttt cag aag ata tat gga aac ccc tgg Val Trp Glu Pro Pro Ile Arg Phe Gln Lys Ile Tyr Gly Asn Pro Trp 405 410 415			1248
atg ccc agg cag aag ttt gct gta ggg gtg ggg tcc tca tgg aga acc Met Pro Arg Gln Lys Phe Ala Val Gly Val Gly Ser Ser Trp Arg Thr 420 425 430			1296
tct gca agg gta gta caa aag gga aat gtt ggg tgg gag ccc cca cac Ser Ala Arg Val Val Gln Lys Gly Asn Val Gly Trp Glu Pro Pro His 435 440 445			1344
aga gtc ccc agt ggg gct cca tct agt aga gct gtg aga aga agt cca Arg Val Pro Ser Gly Ala Pro Ser Ser Arg Ala Val Arg Arg Ser Pro 450 455 460			1392
cca tcc tcc aga ctc cag aag ggt aga tcc act gac agc ttg cag cat Pro Ser Ser Arg Leu Gln Lys Gly Arg Ser Thr Asp Ser Leu Gln His 465 470 475 480			1440
gtg cct gaa aaa tcc aca gac act cag tgc cag cct gtg aaa gca gca Val Pro Glu Lys Ser Thr Asp Thr Gln Cys Gln Pro Val Lys Ala Ala 485 490 495			1488
ggg atg gag tct gta ccc tac aaa acc gta gtg gca gag ctg acc aag Gly Met Glu Ser Val Pro Tyr Lys Thr Val Val Ala Glu Leu Thr Lys 500 505 510			1536
acc gtg gga atc tac ctc ttg cat tgt cat gac ctg gac gtg aga cat Thr Val Gly Ile Tyr Leu Leu His Cys His Asp Leu Asp Val Arg His 515 520 525			1584
gga gtc aaa aga gat cat ttt gga gct tta aga ttt gac tgc ccc act Gly Val Lys Arg Asp His Phe Gly Ala Leu Arg Phe Asp Cys Pro Thr 530 535 540			1632

530	535	540	
gga ttt cgg act tat atg ggg ccc gta ccc ctt tgt ttt ggc caa ttt			1680
Gly Phe Arg Thr Tyr Met Gly Pro Val Pro Leu Cys Phe Gly Gln Phe			
545	550	555	560
ttt cca ttt gga act gcc gta ttt acc caa tgc ctg tac ctc cat tgt			1728
Phe Pro Phe Gly Thr Ala Val Phe Thr Gln Cys Leu Tyr Leu His Cys			
	565	570	575
atg			1731
Met			

<210> 6  
 <211> 577  
 <212> PRT  
 <213> Homo sapiens

<400> 6  
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 1 5 10 15  
 Lys Cys Cys Ile Gly Glu Met Gly Tyr Met Arg Val Thr Met Gly Arg  
 20 25 30  
 Val Gly Ser Trp Arg Glu Leu Gly Lys Pro Ser Gly Ile Trp Glu Met  
 35 40 45  
 Ala Gly Asp Thr Glu Val Lys Lys Thr Gly Phe Leu Gln Glu Leu Thr  
 50 55 60  
 Phe Gln Gln Glu Pro Gly Ile Ser Ser Ser Pro Ser Cys Ser Arg Ser  
 65 70 75 80  
 Cys His Val Thr Pro Ala Pro Pro Ala Ser Ser Ala Ile Ile Val  
 85 90 95  
 Arg Phe Leu Arg Pro Ser Pro Glu Ala Asp Ala Ser Ser Met Leu Ile  
 100 105 110  
 Ala Gln Ser Val Glu Pro Ile Val Val Ile Pro Val Leu Ile Thr Ala  
 115 120 125  
 Val Ile Glu His Val Glu Val Ala Gly Pro Pro Ala His Pro Arg Pro  
 130 135 140  
 Pro Glu Glu Val Gly Pro Pro Gly Ala Pro Gly Leu Pro Gln Tyr Thr  
 145 150 155 160  
 Gly Glu Ile Ser Glu Met Thr Lys Cys Pro Cys Pro Asp Ile Glu Arg  
 165 170 175  
 Ser Ala Phe Thr Val Lys Leu Ser Gly Lys Leu Pro Leu Pro Phe Lys  
 180 185 190  
 Pro Ile Ile Phe Thr Gly Val Leu Tyr Asn Ala Gln Arg Asp Leu Lys  
 195 200 205  
 Glu Ala Met Gly Val Phe Ala Cys Arg Val Pro Gly Asn Tyr Tyr Ser  
 210 215 220  
 Ser Phe Asp Val Glu Leu His His Cys Lys Val Asn Ile Trp Leu Met  
 225 230 235 240  
 Arg Lys Gln Ile Leu Ala Asn Lys Glu Glu Ile Ser Lys Gln Gln Ser  
 245 250 255  
 Ile Gln Glu Val Thr Trp Val Leu Leu Lys Ala Phe Ser Phe Ile Arg  
 260 265 270  
 Glu Ala Glu His Lys Ser Ser Glu Asn Leu His Pro Asp Asn Val Ile  
 275 280 285  
 Lys Lys Lys Asn Pro Phe Ser Glu Gly Lys Phe Lys Leu Ala Ala Glu  
 290 295 300  
 Ile Cys Ile Cys Asn Glu Glu Leu Asn Val Asn Pro Gln Asp Asn Gly  
 305 310 315 320  
 Glu Asn Ile Ser Trp Thr Cys Gln Arg Ser Ser Gln Gln Ser Ile Lys  
 325 330 335  
 Ser Leu Ala Trp Arg Pro Arg Arg Lys Trp Phe Cys Gly Thr Gly Pro



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<210> 7
<211> 1731
<212> DNA
<213> Artificial Sequence
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<221> misc_feature
<222> (1)...(1731)
<223> n = A,T,C or G
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<400>	7					
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aarccnwsng	gnathtggga	ratggcnggn	gayacngarg	tnaaraarac	nggnnttytn	180
cargarytna	cnttycarca	rgarcenggn	athswnsw	snccnwsntg	ywsnmgnwsn	240
tgycaygtna	cncncncng	ncncncngn	wsnwsngcna	thathgtng	nttyytnmgn	300
ccnwsnccng	argcngaygc	nwsnwsnatg	ytnathgcnc	arwsngtnga	rccnathgt	360
gtnathccng	tnytnathac	ngcngtnath	garcaytng	argtngcngg	ncncncngcn	420
cayccnmgnc	cncncgarga	rgtnggncn	ccngggcngc	cnggnytncc	ncartayacn	480
ggngarathw	snargaratg	naartgyccn	tgycngcng	thgarngnws	ngcnttya	540
gtnaarytnw	sgngnaaryt	ncnnytnccn	tyaarcena	thathtyac	ngngntnytn	600
tayaaygcnc	armngayyt	naargargcn	atgggngtnt	tygcntgymg	ngtnccnggn	660
aaytaytayw	snwsnttyga	ygtngarytn	caycaytgya	argtnaayat	htggytnatg	720
mgnaarcara	thytngcnaa	yaargargar	athwsnaarc	arcarwsnat	hcargargtn	780
acntgggtny	tnytnaargc	nttywsntty	athmgngarg	cngarcayaa	rwsnwsngar	840
aayytncayc	cngayaaygt	nathaaaraa	aaraayccnt	tywsngargc	naarttyaar	900
ytngcngcng	arathtgyat	htgyaaygar	garytnaayg	tnaayccnca	rgayaaygg	960
garaayathw	sntggacntg	ycarmgnwsn	wsncarcarw	snathaarws	nytnngcntgg	1020

mgncnmgm	gnaartggtt	ytgyggnaen	ggncnggnw	snytntgytg	ygtnccn	1080
mgngayytng	tnccntgygt	nccngtnaay	wsngcngtng	cnwsngargg	ngcnwsnccn	1140
aarcntggc	arytnccnws	nggngtngar	ccngtnggng	cnaaraarws	nmgnathgar	1200
gtntgggarc	cncnathmg	nttycaraar	athtayggna	ayccntggat	gccnmgnar	1260
aarttygcng	tnggngtngg	nwsnwsntgg	mgnacnwsng	cnmgngtngt	ncaraarggn	1320
aaygtnggnt	gggarccncc	ncaymgngtn	ccnwsnggng	cncnwsnws	nmgngcngtn	1380
mgnmgwnsnc	cncnwsnws	nmgnytnar	aarggnmgw	snacngayws	nytnarcar	1440
gtncngara	arwsnacnga	yacncartgy	carcngtna	argcngcngg	natggarwsn	1500
gtncntaya	aracngtngt	ngcngarytn	acnaaracng	tnggnathta	yytnytnay	1560
tgycaygayy	tngaygtngm	ncayggngtn	aarmngayc	ayttyggngc	nytnmgntty	1620
gaytgyccna	cnggnttymg	nacntayatg	ggncngtnc	cnytntgytt	yggnartty	1680
ttyccnttyg	gnacngcngt	nttyacncar	tgyytntayy	tnaytgyat	g	1731